

Figure 1

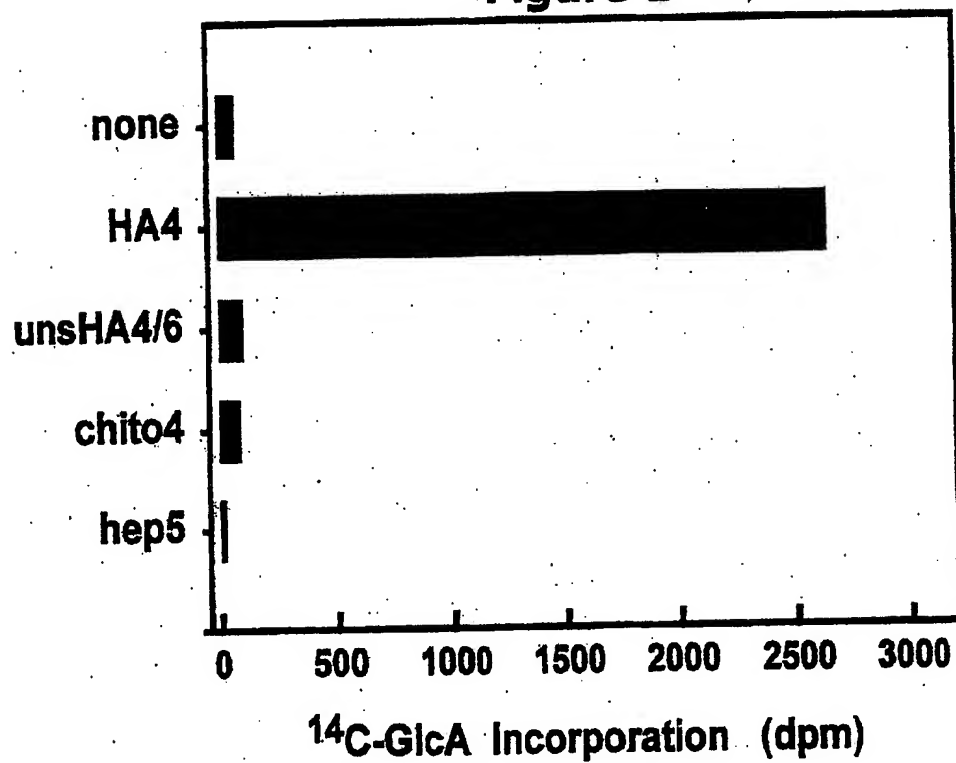
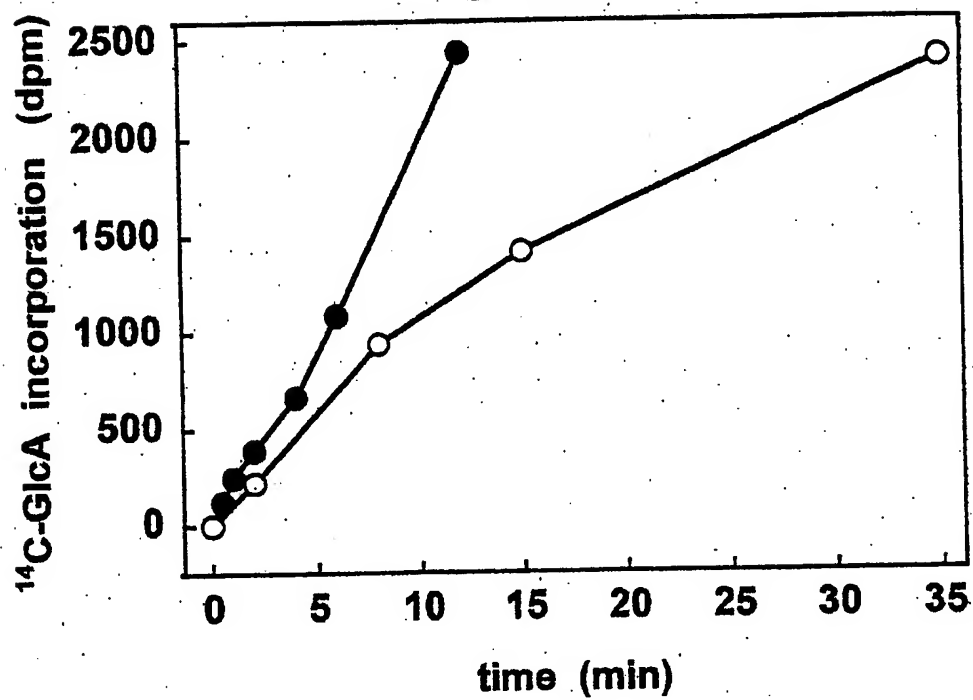
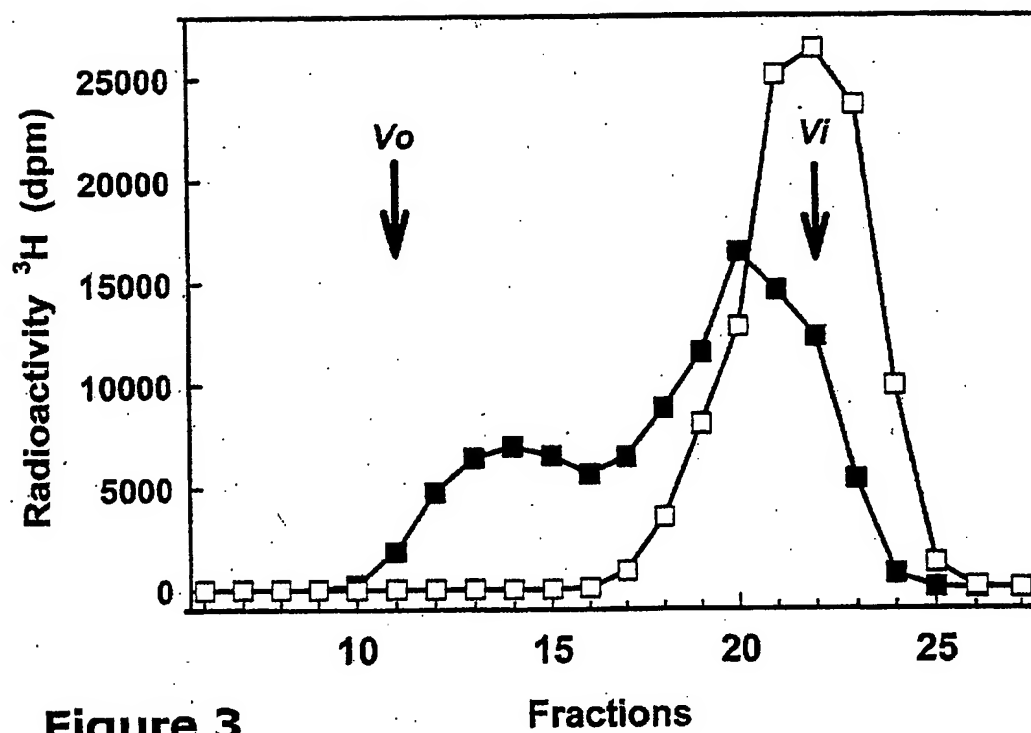


Figure 2





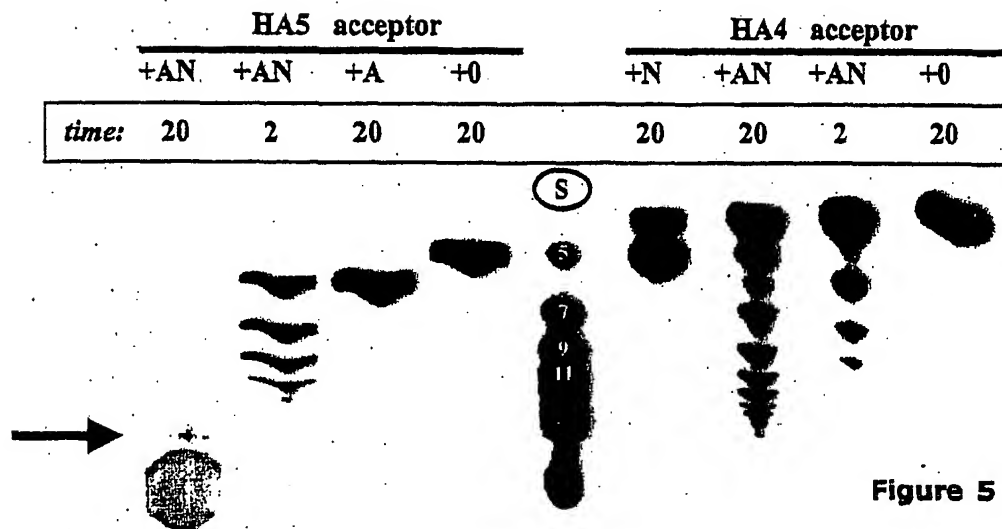


Figure 5

Ion Gel Filtration

Ex Fractions

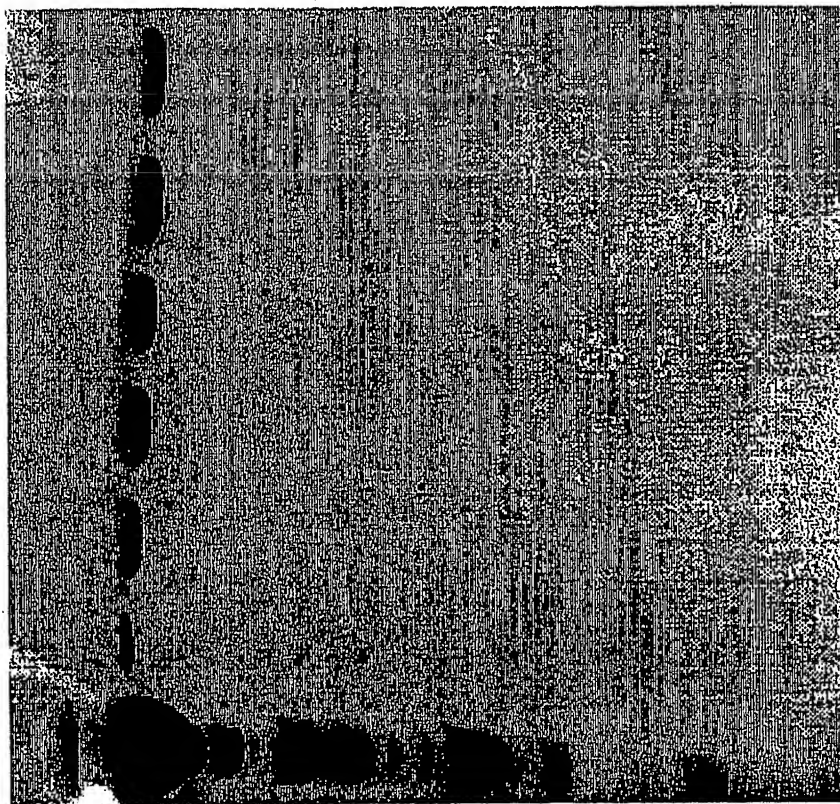
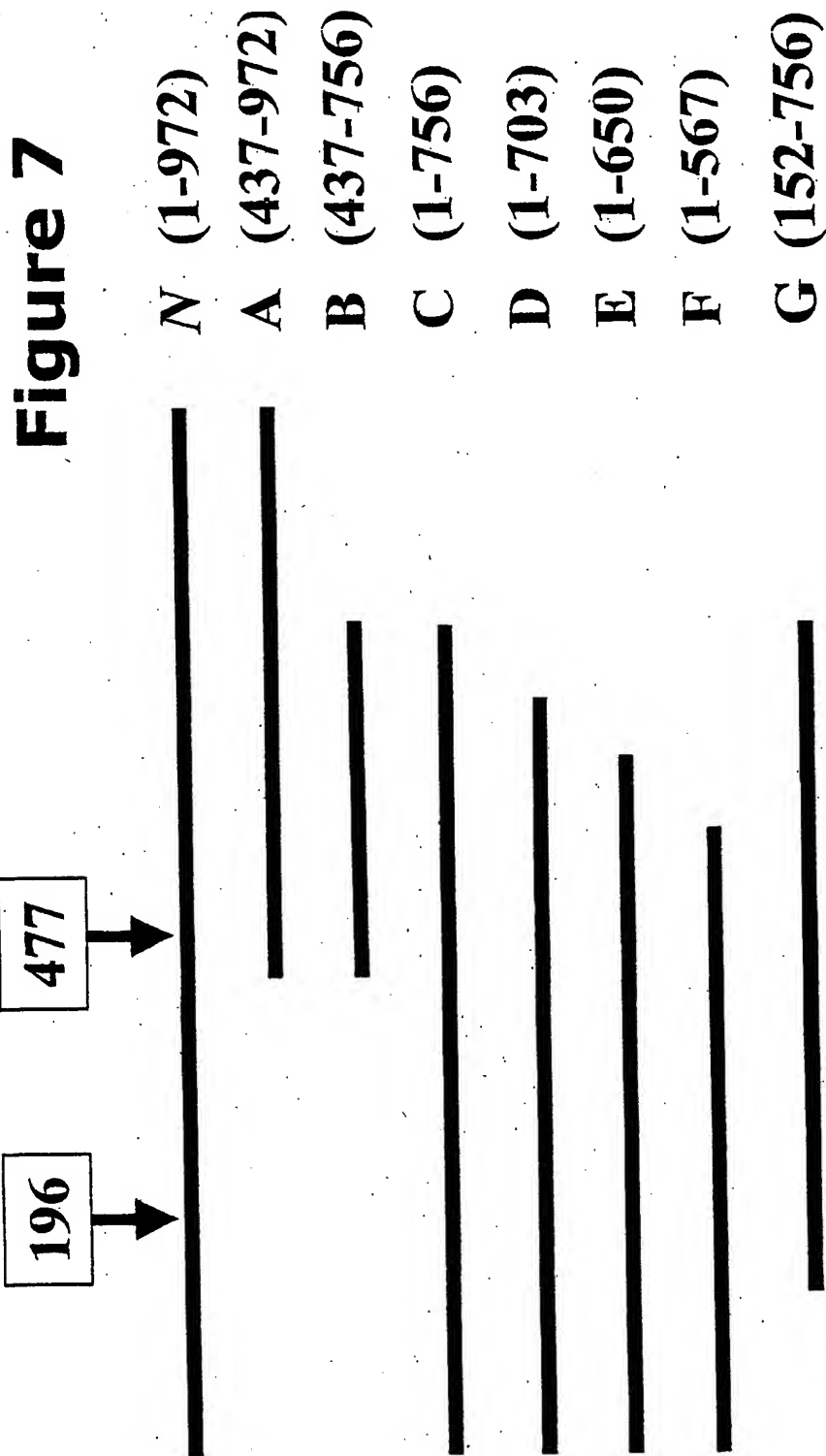


Figure 6



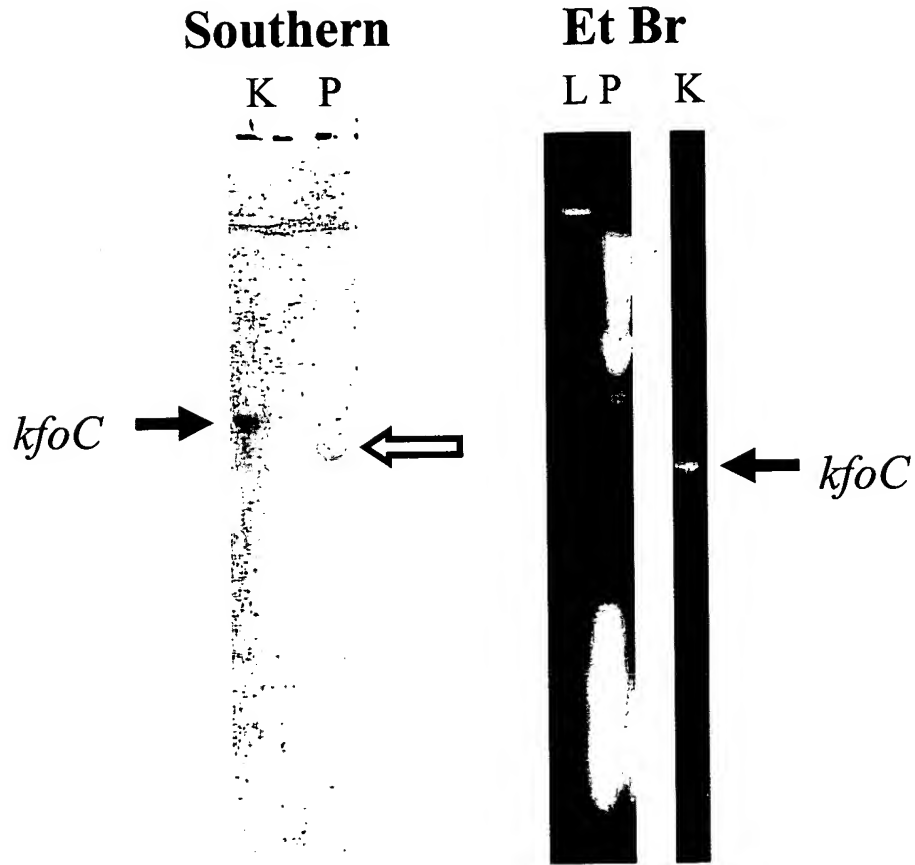


FIG. 8

Figure 9

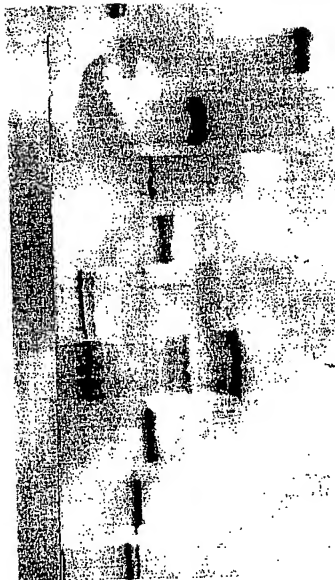


Figure 10

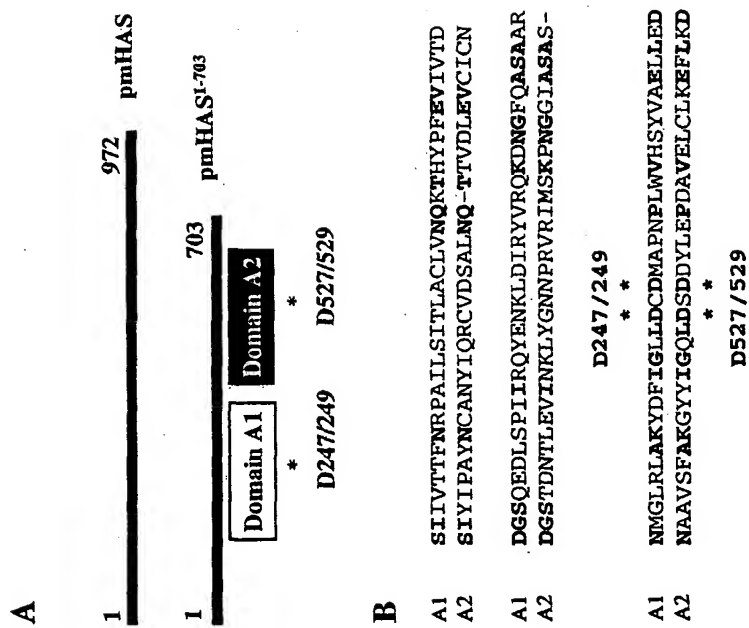


Figure 11

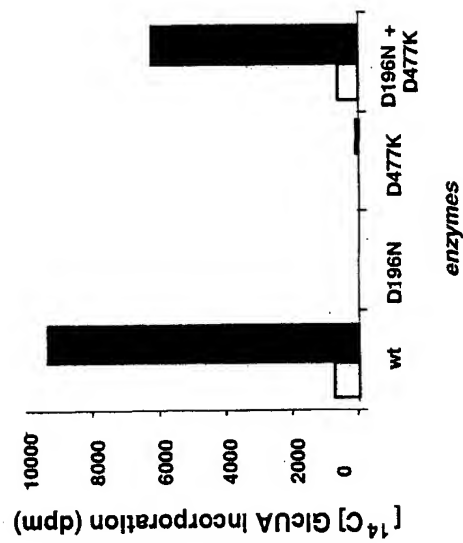


Figure 12

pmCS	1	MNTLSQAIKA	YNSNDYELAL	KLFKSAETI	GRKIVETQII	KCKEKLSTNS	50
pmHAS		-----	-----Q-----	-----I-----	-----T-----	-----AHP-----	
pmCS	51	YVS-----	EDKKNVCDSS	SDIATQILL	SNVKELTISE	SEKNSLAKKW	100
pmHAS		S-NSAHLNVN	KEE-VN----	P-----	-----V--D-----	-----T-----	
pmCS	101	KBITGKKSEN	AEIRKVELVP	KDFPKDIVLA	FLPDHVNDFT	WYKNNRKKSLG	150
pmHAS		-LL-E-----	--V-A-A----	-----	-----	---K---R---	
pmCS	151	IKFVNKNIGL	SLIPTFNRS	RILDITLACL	VNOKTNYEPE	VVVADDGSEK	200
pmHAS		---EQHV---	---VT---P	A--S-----	-----H-----	-I-T---Q-	
pmCS	201	NELTIQRYE	QRLDIKYVRO	KDYGYQLCAV	RNLGLRTAKY	DYVSILDCDM	250
pmHAS		D-SP-IRQ--	N---R----	--N-F-RS-A	--M--L---	--IGL---	
pmCS	251	APQQLWVHSY	LTELLEDNDI	VLIGPRKYVD	THNITAEQFL	NDPYLIESLP	300
pmHAS		--NP-----	VA-----D-L	TI-----I-	-QH-DEKD--	-NAS-L----	
pmCS	301	ETATNNNPSI	TSKNISLDW	RLNHTAKTON	LRICDSPFRY	FVAGNVAFSK	350
pmHAS		--VK---SVAA	KGE-TV----	---Q-T--E-	---S-----T	-A-----A-	
pmCS	351	EWLNKVGHPD	EETNNWGGED	VEFGYALEAK	GCEFRVIDGG	MAIHQEPFGK	400
pmHAS		K-----S-F--	-----	-----R-	-S--KT--I	--Y-----	
pmCS	401	ENETEREACK	SITLKIYKEK	VPYTKRLFP	IEDSHIRIP	LVSIVIPAYN	450
pmHAS		-----D----	N---D-MR--	-----	-----N-V-	-----	
pmCS	451	CANYIQRCVD	SALNQTVDL	EVCICNDGST	DNTLEVINKL	YGNNPRVRIM	500
pmHAS		-----	-----	-----	-----	-----	
pmCS	501	SKFNGGIASA	SNAAVSFARG	YYIGQLDSDD	YLEPDVAVLC	EKEFLDKTTL	550
pmHAS		-----	-----	-----	-----	-----	
pmCS	551	ACVYITNRNV	NPDGSLIANG	YNWPEFSREK	LTTAMLAHHT	RMFTIRAWHL	600
pmHAS		-----	-----	-----	-----	-----	
pmCS	601	TGTFNMENIEN	AVDYDMFLKL	SEVGKFKHIN	KICYNRVLHG	DNTSIXKLG	650
pmHAS		-----K----	-----	-----	-----	-----	
pmCS	651	QKKNHFFVVN	QSLNRQGTNY	YNYDREDDLD	ESRKYIFNKT	AEYQRENDML	700
pmHAS		-----	-----T-	-----E-	-----	-----I-I-	
pmCS	701	KDLKLIONKD	AKIAVSITYP	NTINGLVKKL	NMITEYNKNI	FVILHVDKN	750
pmHAS		--I-I-----	-----	-----	-----	---V-----	
pmCS	751	HLTFDIKKEI	LAFYHKHQVN	ILLNNDISYY	TSNRLIKTEA	HLNINIKLSQ	800
pmHAS		-----	-----	-----	-----	-----	
pmCS	801	LNLNCEYIIF	DNHDSLFVK	DSYAYMKKYD	VGMNESALTH	DWIEKINAHF	850
pmHAS		-----	-----	-----	-----	-----	
pmCS	851	PFKKLIKTYF	NDNDRSMNV	KGASQGMFMK	YALPHELLTI	IKKVITSQCS	900
pmHAS		-----	-----K----	-----T	---A-----	-----	
pmCS	901	IDSVPEYNTE	DINQFALLI	LEKKIGHVFN	KTSITLYMPW	ERKLQWTEQ	950
pmHAS		-----	-----	-----	-----	-----	
pmCS	951	IQBAKKGNI	PVKRFIINSI	TL			972
pmHAS		-E---R-----	-----	---			

Figure 13

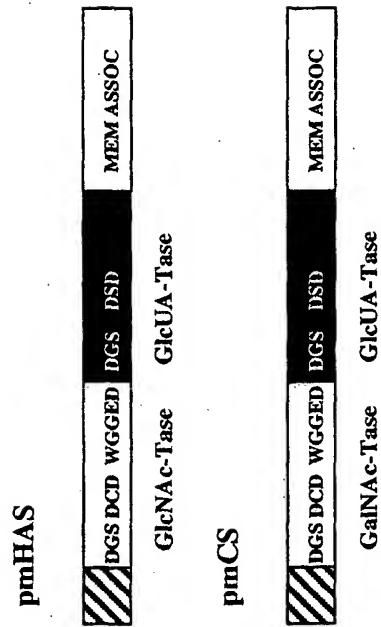


Figure 14

91	140
APPLVSIIMTSHNTEKFEASINSLLOTTYNNEVIVVDDYSTDKTFQIA	
GKDLVSIIMSVFENSEDTIAYSLHLLNQTYENIEILVCDDCSSDKSLEII	
...LVSIIM*.N*.E..I..S..SLL.QTY#N.E!.V.DD.S*DK*.#I.	
141	190
SRIANSTSKVKTFRINSLNLTGYFAKNTGILKSKGDIFFQBSDDVCHHER	
KSIAYSSSRVKVYSSRKNQGPYNIRNELIKKAHGNFIFQDADDLSHPER	
..IA.S*S*VK.%....N.G.Y...N..I.K..G#.I.FQD.DD..H.ER	
191	240
IERCVNALLSNKDNIAVRCAYSRINLETQNIKVNNDKYLGLITLGVYR	
IQRQVEVLRNNKAVICM.ANWIRVASNGKIQFFYDDKATRMSVSSMIKK	
I#R.V#.L..NK..I.....R!..#.....#D....*\$...!*...!.*	
441	490
YITCDDDIRYPADYINTMIKKINKYND.KAAIGLHGVIFPSRVNKFSSD	
IVLTDDDDIIYPPDYVEKMLNFYNSEAFENCIVGIHGCIIYIDAFDGD.QSK	
..!..DDDI.YP.DY!#M....N.%.....!G.HG.I%.....#.....S.	
491	540
RIVYNFQKTFRKDTAVNLTGTVAFRVSIENKFSLSDFEHPGMVDIYFS	
RKVFSFTQGLLRPRVNVQLGTGTVFLKADQLPSLKYMDGSQR.FVDVRES	
R.V%.F.....*.VN.LGTGTV.*.....D.....VD!..FS	

Figure 14 cont'd

1

617



Figure 15A

	1	10	20	30	40	50	60	70
Kf1C								
HSA1	GKDLVSLHSVFNSEDIAYLSHLLNQTYENIELVCDDCSSDKSELIKSJAYSRRVKYSSRKHQG							
kf1A	APPLYSLIHTSHNTEKFIEASHLSLLOQYNNLEVTVDYDSDTKTFQIASRIANSTSKVKTFRLSNLG							
HSA2	MIVANNASSYPPRKKELVHSIQSLHRY-QDNINCLNEFEETPEELDGFSLNPVI-----POKYDYDVG							
Consensus	IPYYNICSPSRKQLQYTIIGVLKHQC-DHFHIYLDGYEVPDFIKKLGNKATVINCNKNESIRDWG							
	.p.v.nl.s.p.r.k.l.y.sl.nq.#.i.i.l.....e.p.l....s.a.vi.....s.k#.g							
	71	80	90	100	110	120	130	140
Kf1C								
HSA1	PYLRLNELIKKAHGFIITFQRADILSHIPERIQRQVEVLRNNKVATICH-AMHIVASNGKIQQFYDDKATR							
kf1A	TYFAKNTGILKSGDIFFQDSUDVCCHIERECYNALLSNKQJAVRVCHAYSRLINLETQNLIKVMWNKYK							
HSA2	KEIF-----PCAKMDMIYLTDDILIYPPDYVEKALMFWNSFALFNCTVINGCTIYIDAFDGD-QSKKKV-							
Consensus	KFTILLEKLIKENKUGYYTICODDIRPADIYINTAIKKINKYND-KAAIGLGHVIFPSRVANKYFESSDIRV-							
	kxi.....lik.ak.d.i....DdBi.gpp#y!#.n.n.ns..d..a..g.hg.i.....n...f.sdr-kv.							
	141	150	160	170	180	190	200	210
Kf1C								
HSA1	MSVSSMIKKOIFAIVGGYRQSILGADTEFYETIVIRYGRESIVRLLOPLILGLAGDSGLTRMKGTALP							
kf1A	LGLTLGVYRKVFNEIGFNCTTKASDDEFYHRILKYKGKRNRLNFLFLPYNTAREDSLFSOH-YEVAD							
HSA2	FSTFGILLRPVVNLG---TGTVFLKHUQLPSLYAHOGSQR-FYDVRFSRYALENEIGHICVPREKNHLR							
Consensus	YMFQKTRKDTAVNLDG--TGTVAFRVYSIFNKFSLSOFEPHGVNDIFYSLCKNNILQVCISRPSNMLI							
	.sf.....k..vvn.lg..tgv.....d.f.....nd.....vd..fs.y...n.i....c.f...#dl.							
	211	220	230	240	250	260	263	
Kf1C								
HSA1	DGYTSQSRREYSOIARQRVLGKSIYSOKDVGRGLSRYGLFKDVSSELIEQ							
kf1A	ENNKKQKTSQARQNYLHEFAQTHMERKFNELKEIFS-FPRTHDALPISEMSK							
HSA2	EVS-SGSHEGLNFTTKKAPLDI-IKETQAIIAGYSKLNLELVYNVEG							
Consensus	EDN-KNT-ETLFHEFQNRUDEQSKLIISNHPWGYSSIIPLAHNANYSELIPC							
	#.n.k.s.e.l...f.....l.....i.....n...gyss.ypll..n.....se....							

Figure 15B

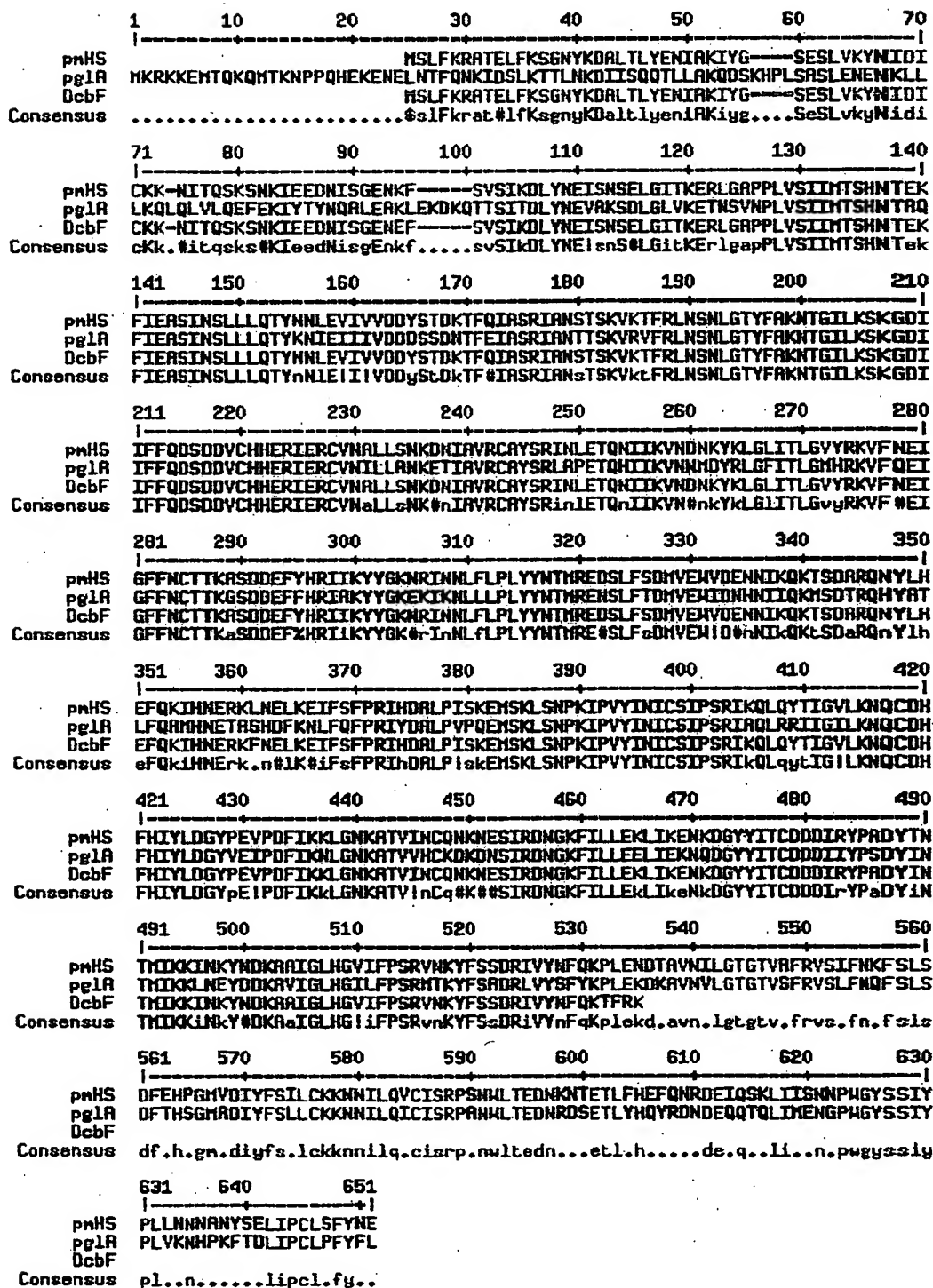


Figure 15C

Multalin version 5.4.1

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Published research using this software should cite

Multiple sequence alignment with hierarchical clustering

F. CORPET, 1988, Nucl. Acids Res., 16 (22), 10881-10890

Symbol comparison table: blosum62

Gap weight: 12

Gap length weight: 2

Consensus levels: high=90% low=50%

Consensus symbols:

! is anyone of IV

\$ is anyone of LM

* is anyone of FY

is anyone of NDQEBZ

MSF: 651 Check: 0

Name: A Len: 651 Check: 612 Weight: 0.58

Name: B Len: 651 Check: 249 Weight: 0.58

Name: pglA Len: 651 Check: 7677 Weight: 1.08

Name: DcbF Len: 651 Check: 7537 Weight: 1.76

Name: Consensus Len: 651 Check: 5816 Weight: 0.00

//

```

      1                                     50
      A2 ..... MSLFKR ATELFKSGNY KDALTLYENI
      B10 ..... MSLFKR ATELFKSGNY KDALTLYENI
      pglA MKRKKEMTQK QMTKNPPQHE KENELNTFQK KIDSLKTTLN KDIISQQTLL
      DcbF ..... MSLFKR ATELFKSGNY KDALTLYENI
      sensus ..... $s1Fkr at#1fKsgny KDaltlyeni

      51                                     100
      A2 AKIYG....S ESLVKYNIDI CKK.NITQSK SNKIEEDNIS GENKF.....
      B10 AKIYG....S ESLVKYNIDI CKK.NITQSK SNKIEEDNIS GENKF.....
      pglA AKQDSKHPLS ASLENENKLL LKQLQLVLQE FEKIYTYNQA LEAKLEKDKQ
      DcbF AKIYG....S ESLVKYNIDI CKK.NITQSK SNKIEEDNIS GENE.....
      Consensus AKiyg....S eSLvkyNidi cKk.#itqsk s#KleedNis gEnkf.....

      101                                    150
      A2 SVSIKDLYNE ISNSELGITK ERLGAPPLVS IIMTSHNTEK FIEASINSLL
      B10 SVSIKDLYNE ISNSELGITK ERLGAPPLVS IIMTSHNTEK FIEASINSLL
      pglA TTSITDLYNE VAKSDLGLVK ETNSVNPLVS IIMTSHNTAQ FIEASINSLL
      DcbF SVSIKDLYNE ISNSELGITK ERLGAPPLVS IIMTSHNTEK FIEASINSLL
      Consensus svSIkDLYNE !snS#LGitK ErlgapPLVS IIMTSHNTek FIEASINSLL

      151                                    200
      A2 LQTYNNLEVI VDDYSTDKT FQIASRIANS TSKVKTFRLN SNLGTYFAKN
      B10 LQTYNNLEVI VDDYSTDKT FQIASRIANS TSKVKTFRLN SNLGTYFAKN
      pglA LQTYKNIEII IVDDSSDNT FEIASRIANT TSKVRVFRN SNLGTYFAKN
      DcbF LQTYNNLEVI VDDYSTDKT FQIASRIANS TSKVKTFRLN SNLGTYFAKN
      Consensus LQTYnN1E!I !VDDyStDkt F#IASRIANS TSKVktFRLN SNLGTYFAKN
  
```

Fig. 15C cont'd

201					250
A2	TGILKSKGDI	IFFQSDDDVC	HHERIERCVN	ALLSNKDNIA	VRCAYSRINL
B10	TGILKSKGDI	IFFQSDDDVC	HHERIERCVN	ALLSNKDNIA	VRCAYSRINL
pg1A	TGILKSKGDI	IFFQSDDDVC	HHERIERCVN	ILLANKETIA	VRCAYSRLAP
DcbF	TGILKSKGDI	IFFQSDDDVC	HHERIERCVN	ALLSNKDNIA	VRCAYSRINL
Consensus	TGILKSKGDI	IFFQSDDDVC	HHERIERCVN	aLLsNK#nIA	VRCAYSRinl
251					300
A2	ETQNIIVND	NKYKLGITL	GVYRKVFNEI	GFFNCTTKAS	DDEFYHRIIK
B10	ETQNIIVND	NKYKLGITL	GVYRKVFNEI	GFFNCTTKAS	DDEFYHRIIK
pg1A	ETQNIIVNN	MDYRLGFITL	GMHRKVQEI	GFFNCTTKGS	DDEFFHRIAK
DcbF	ETQNIIVND	NKYKLGITL	GVYRKVFNEI	GFFNCTTKAS	DDEFYHRIIK
Consensus	ETQNIIVN#	nkYkLGITL	GvyRKVF#EI	GFFNCTTKaS	DEFE#HRIiK
301					350
A2	YYGKNRINN	FLPLYNTMR	EDSLFSDMVE	WVDENNIKQK	TSDARONYLH
B10	YYGKNRINN	FLPLYNTMR	EDSLFSDMVE	WVDENNIKQK	TSDARONYLH
pg1A	YYGKEKIKN	LLPLYNTMR	ENSLFTDMVE	WIDNHNIIQK	MSDTRQHYAT
DcbF	YYGKNRINN	FLPLYNTMR	EDSLFSDMVE	WVDENNIKQK	TSDARONYLH
Consensus	YYGK#rInNL	fLPLYNTMR	E#SLFSDMVE	WID#nNikQK	tSDaRQnYlH
351					400
A2	EFQKIHNERK	LNELKEIFSF	PRIHDALPIS	KEMSKLSNPK	IPVYINICSI
B10	EFQKIHNERK	LNELKEIFSF	PRIHDALPIS	KEMSKLSNPK	IPVYINICSI
pg1A	LFQAMHNETA	SHDFKNLFQF	PRIYDALPVP	QEMSKLSNPK	IPVYINICSI
DcbF	EFQKIHNERK	FNELKEIFSF	PRIHDALPIS	KEMSKLSNPK	IPVYINICSI
Consensus	efQkIHNErk	.n#lK#iFsf	PRIhDALP!s	kEMSKLSNPK	IPVYINICSI
401					450
A2	PSRIKQLQYT	IGVLKNQCDH	FHIYLDGYPE	VPDFIKKLGN	KATVINCONK
B10	PSRIKQLQYT	IGVLKNQCDH	FHIYLDGYPE	VPDFIKKLGN	KATVINCONK
pg1A	PSRIAQLRRI	IGILKNQCDH	FHIYLDGYVE	IPDFIKKLGN	KATVVHCKDK
DcbF	PSRIKQLQYT	IGVLKNQCDH	FHIYLDGYPE	VPDFIKKLGN	KATVINCONK
Consensus	PSRIkQLQyt	IG!LKNQCDH	FHIYLDGYpe	!PDFIKkLGN	KATV!nCq#K
451					500
A2	NESIRDNGKF	ILLEKLIKEN	KDGYIITCDD	DIRYPADYTN	TMIKKINKYN
B10	NESIRDNGKF	ILLEKLIKEN	KDGYIITCDD	DIRYPADYIN	TMIKKINKYN
pg1A	DNSIRDNGKF	ILLEELIEKN	QDGYIITCDD	DIIYPSDYIN	TMIKKLNEYD
DcbF	NESIRDNGKF	ILLEKLIKEN	KDGYIITCDD	DIRYPADYIN	TMIKKINKYN
Consensus	##SIRDNGKF	ILLEkLIken	kDGYIITCDD	DirYPaDYiN	TMIKKiNky#
501					550
A2	DKAAIGLHGV	IFPSRVNKYF	SSDRIVYNFQ	KPLENDTAVN	ILGTGTVAFR
B10	DKAAIGLHGV	IFPSRVNKYF	SSDRIVYNFQ	KPLENDTAVN	ILGTGTVAFR
pg1A	DKAVIGLHGI	LFPSRMTKYF	SADRLVYSFY	KPLEKDKAVN	VLGTGTVSFR
DcbF	DKAAIGLHGV	IFPSRVNKYF	SSDRIVYNFQ	KTFRK.....
Consensus	DKAAIGLHG!	iFPSRvnKYF	SsDRiVYnFq	Kplekd.avn	.lgtgtv.fr
551					600
A2	VSIFNKFSLS	DFEHPGMVDI	YFSILCKKNN	ILQVCISRPS	NWLTEDNKNT
B10	VSIFNKFSLS	DFEHPGMVDI	YFSILCKKNN	ILQVCISRPS	NWLTEDNKNT
pg1A	VSLFNQFSLS	DFTHSGMADI	YFSLLCKKNN	ILQICISRPA	NWLTEDNRDS
DcbF
Consensus	vs.fn.fsIs	df.h.gm.di	yfs.lckknn	ilq.cisrp.	nwltedn...

Fig. 15C c nt'd

	601		650
A2	ETLFHEFQNR	DEIQSKLIIS	NNPWGYSSIIY PLLNNNANYS ELIPCLSFYN
B10	ETLFHEFQNR	DEIQSKLIIS	NNPWGYSSIIY PLLNNNANYS ELIPCLSFYN
pglA	ETLYHQYRDN	DEQQTQLIME	NGPWGYSSIIY PLVKNHPKFT DLIPCLPFYF
DcbF
Consensus	etl.h.....	de.q..li..	n.pwgyssiy pl..n..... .lipcl.fy.

	651
A2	E
B10	E
pglA	L
DcbF	.
Consensus	.

Figure 15D

Multalin version 5.4.1

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Published research using this software should cite

Multiple sequence alignment with hierarchical clustering

F. CORPET, 1988, Nucl. Acids Res., 16 (22), 10881-10890

Symbol comparison table: blosum62

Gap weight: 12

Gap length weight: 2

Consensus levels: high=90% low=50%

Consensus symbols:

! is anyone of IV

\$ is anyone of LM

% is anyone of FY

is anyone of NDQEBZ

MSF: 651 Check: 0

Name: pmHS Len: 651 Check: 612 Weight: 0.75

Name: pgla Len: 651 Check: 7677 Weight: 0.75

Name: DcbF Len: 651 Check: 7537 Weight: 1.49

Name: Consensus Len: 651 Check: 5816 Weight: 0.00

//

```

1                                     50
pmHS .....MSLFKR ATELFKSGNY KDALTLYENI
pgla MKRKKKEMTQK QMTKNPPQHE KENELNTFQN KIDSLKTTLN KDIIISQQTLL
DcbF .....MSLFKR ATELFKSGNY KDALTLYENI
Consensus .....$sLFkr at#lFksgny KDaltlyeni

51                                     100
pmHS AKIYG....S ESLVKYNIDI CKK.NITQSK SNKIEEDNIS GENKF.....
pgla AKQDSKHPLS ASLENENKLL LKQLQLVLQE FEKIYTYNQA LEAKLEKDKQ
DcbF AKIYG....S ESLVKYNIDI CKK.NITQSK SNKIEEDNIS GENE.....
Consensus AKIyg....S eSLvkyNidi cKk.#itqsk s#KieedNis gEnkf.....

101                                    150
pmHS SVSIKDLYNE ISNSELGITK ERLGAPPLVS IIMTSHNTEK FIEASINSLL
pgla TTSITDLYNE VAKSDLGLVK ETNSVNPLVS IIMTSHNTAQ FIEASINSLL
DcbF SVSIKDLYNE ISNSELGITK ERLGAPPLVS IIMTSHNTEK FIEASINSLL
Consensus svSikDLYNE !sn$LGitK ErlgapPLVS IIMTSHNtek FIEASINSLL

151                                    200
pmHS LQTYNNLEVI VDDYSTDKT FQIASRIANS TSKVKTFRNL SNLGTYFAKN
pgla LQTYKNIEII IVDDSSDNT FEIASRIANT TSKVRVFRNL SNLGTYFAKN
DcbF LQTYNNLEVI VDDYSTDKT FQIASRIANS TSKVKTFRNL SNLGTYFAKN
Consensus LQTYnNle!I !VDDyStDkt F#IASRIANS TSKVktFRNL SNLGTYFAKN

201                                    250
pmHS TGILKSKGDI IFFQSDDDVC HHERIERCVN ALLSNKDNIA VRCAYSRLNL
pgla TGILKSKGDI IFFQSDDDVC HHERIERCVN ILLANKETIA VRCAYSRLAP
DcbF TGILKSKGDI IFFQSDDDVC HHERIERCVN ALLSNKDNIA VRCAYSRLNL
Consensus TGILKSKGDI IFFQSDDDVC HHERIERCVN aLLsNK#nIA VRCAYSRLnl

251                                    300
pmHS ETQNIIVKND NKYKLGILITL GYRKVFNEI GFFNCTTKAS DDEFYHRIIK
pgla ETQHIIKVNND MDYRLGFITL GMHRKVFQEI GFFNCTTKGS DDEFFHRIAK
DcbF ETQNIIVKND NKYKLGILITL GYRKVFNEI GFFNCTTKAS DDEFYHRIIK
Consensus ETQnIIVKND# nkYKLGILITL GvyRKVF#EI GFFNCTTKaS DDEF#HRIiK

```

Figure 15D

	301		350
pmHS	YYGKNRINNL	FLPLYNTMR	EDSLFSDMVE WVDENNIKQK TSDARQNYLH
pglA	YYGKEKIKNL	LLPLYNTMR	ENSLFTDMVE WIDNHNIIQK MSDTRQHYAT
DcbF	YYGKNRINNL	FLPLYNTMR	EDSLFSDMVE WVDENNIKQK TSDARQNYLH
Consensus	YYGK#rInNL	flPLYNTMR	E#SLFsDMVE WID#nNIkQK tSDaRQnYlH
	351		400
pmHS	EFQKIHNERK	LNELKEIFS	PRIHDALPIS KEMSKLSNPK IPVYINICSI
pglA	LFQAMHNETA	SHDFKNLFQF	PRIYDALPVP QEMSKLSNPK IPVYINICSI
DcbF	EFQKIHNERK	FNELKEIFS	PRIHDALPIS KEMSKLSNPK IPVYINICSI
Consensus	eFQkiHNErk	.n#lK#iFsF	PRIHDALP!s KEMSKLSNPK IPVYINICSI
	401		450
pmHS	PSRIKQLQYT	IGVLKNQCDH	FHIYLDGYPE VPDFIKKLGN KATVINCONK
pglA	PSRIAQLRRI	IGILKNQCDH	FHIYLDGYVE IPDFIKNLGN KATVVHCKDK
DcbF	PSRIKQLQYT	IGVLKNQCDH	FHIYLDGYPE VPDFIKKLGN KATVINCONK
Consensus	PSRIkQLqyt	IG!LKNQCDH	FHIYLDGYpe !PDFIKKLGN KATV!nCq#K
	451		500
pmHS	NESIRDNGKF	ILLEKLIKEN	KDGYITCDD DIRYPADYTN TMIKKINKYN
pglA	DNSIRDNGKF	ILLEELIEKN	QDGYITCDD DIIYPSDYIN TMIKKLNEYD
DcbF	NESIRDNGKF	ILLEKLIKEN	KDGYITCDD DIRYPADYIN TMIKKINKYN
Consensus	##SIRDNGKF	ILLEkLiken	kDGYITCDD DirYPaDYiN TMIKKiNkY#
	501		550
pmHS	DKAAIGLHGV	IFPSRVNKYF	SSDRIVYNFQ KPLENDTAVN ILGTGTVAFR
pglA	DKAVIGLHGI	LFPSRMTKYF	SADRLVYSFY KPLEKD KAVN VLGTGTVSFR
DcbF	DKAAIGLHGV	IFPSRVNKYF	SSDRIVYNFQ KTFRK.....
Consensus	DKAAaIGLHG!	iFPSRvnKYF	SsDRiVYnFq Kplekd.avn .lgtgtv.fr
	551		600
pmHS	VSIFNKFSLS	DFEHPGMVDI	YFSILCKKNN ILQVCISRPS NWLTEDNKNT
pglA	VSLFNQFSLS	DFTHSGMADI	YFSLLCKKNN ILQICISRPA NWLTEDNRDS
DcbF
Consensus	vs.fn.fsls	df.h.gm.di	yfs.lckknn ilq.cisrp. nwltedn...
	601		650
pmHS	ETLFHEFQNR	DEIQSKLIIS	NNPWGYSSII PLLNNNANYS ELIPCLSFYN
pglA	ETLYHQYRDN	DEQQTQLIME	NGPWGYSSII PLVKNHPKFT DLIPCLPFYF
DcbF
Consensus	etl.h.....	de.q..li..	n.pwgyssiy pl..n..... .lipcl.fy.
	651		
pmHS	E		
pglA	L		
DcbF	.		
Consensus	.		

Figure 16

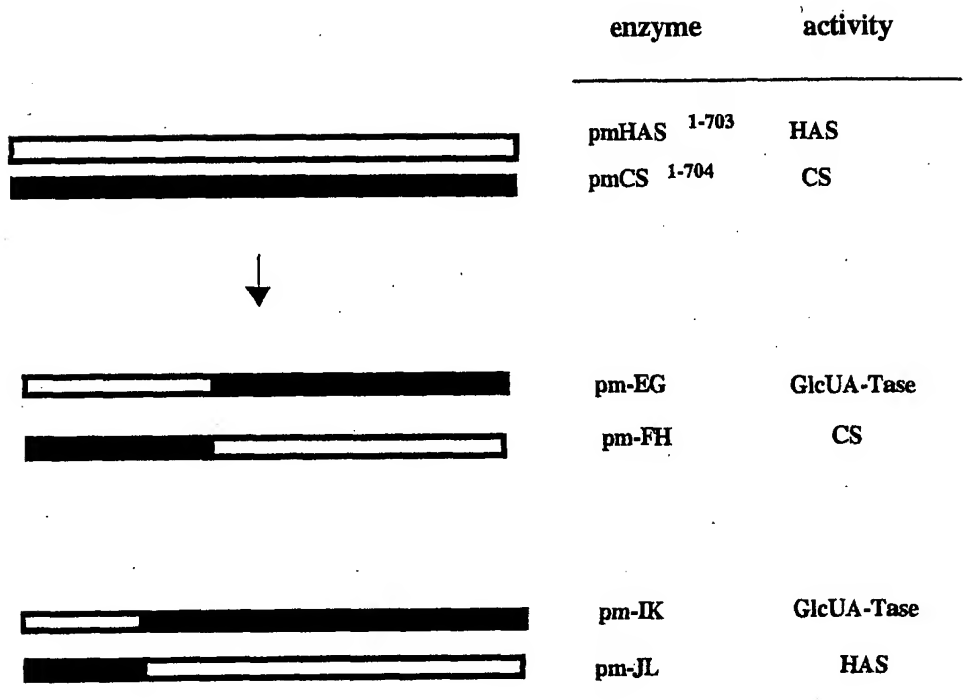


Figure 17

	211	220	230	240	250
	-----+-----+-----+-----+				
PnHAS	NKLDIRYYRQKDNQGFQASARNMGLRLAKYDFIGLLDCDH				
PnCS	QKLDIKYYRQKDYGYQLCAVRNLGLRTAKYDFYSILDCDH				
Turkey	EKLDIKYYRQKDYGYQLCAVRNLGLRTAKYDFYSILDCDH				
Goose	YDIKYYRQKDYGYQLCAVRNLGLRTAKYDFYSILDC				
Sea-lion	KYYRQKDYGYQLCAVRNLGLRTAKYDFYSILDC				
Consensus	...dikYYRQKDYGYQLCAVRNLGLRTAKYDF!siLDC...				
mutant 1		★			
mutant 2			★		
mutant 3			★		
mutant 4		★	★		
mutant 5		★	★		
mutant 6			★★		
mutant 7		★	★★		
mutant 8				★	
mutant 9				★★★	

Figure 18

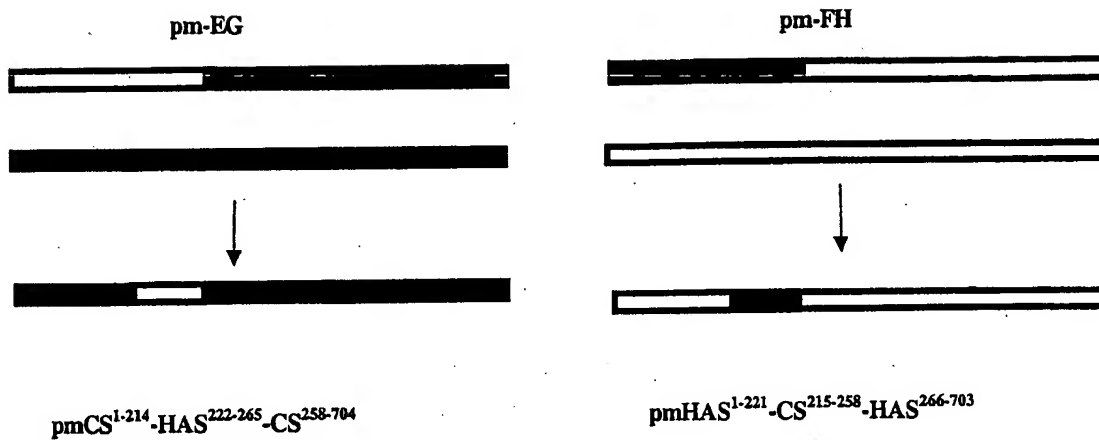


Figure 19



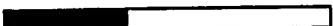





enzyme	activity		
	HAS	CS	GlcUA-Tase
 pm-BD	-	+	<input checked="" type="checkbox"/>
 + pm-AC	+	-	<input checked="" type="checkbox"/>
 + pm-FH	-	+	+
 pm-EG	-	-	+
 Pm-JL	+	-	+
 pm-IK	-	-	+
 pmCHC	+	+	+
 pmHCH	not expressed		

FIGURE 20



FIGURE 21

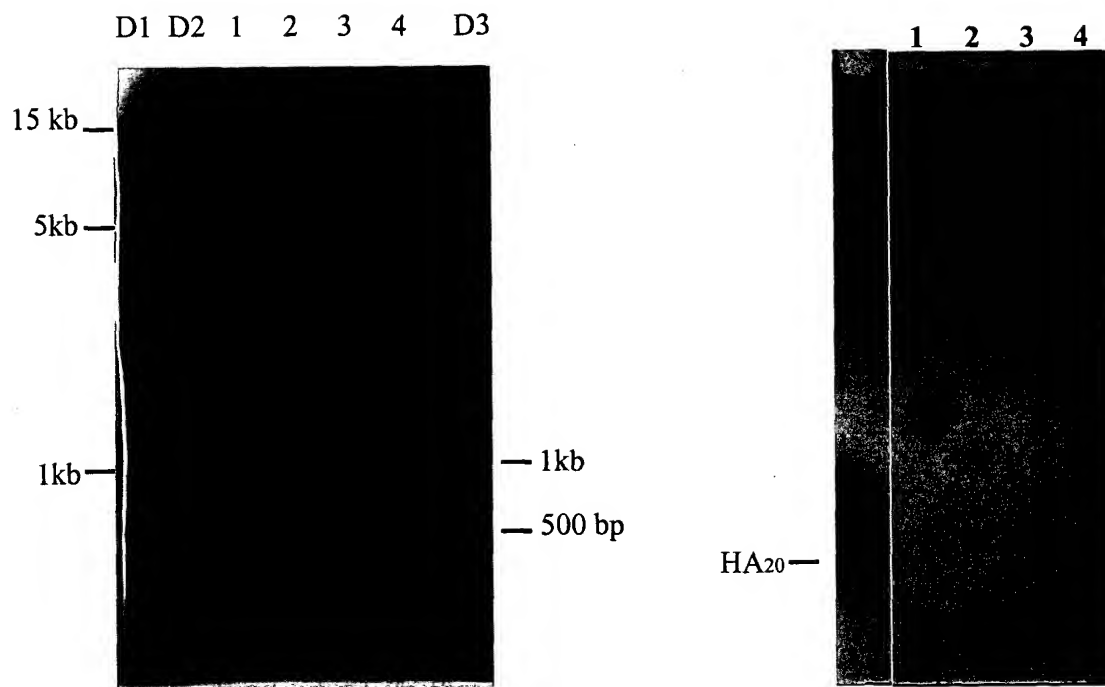


FIGURE 22.
Model of *Pasteurella*
Synthase Polymerization

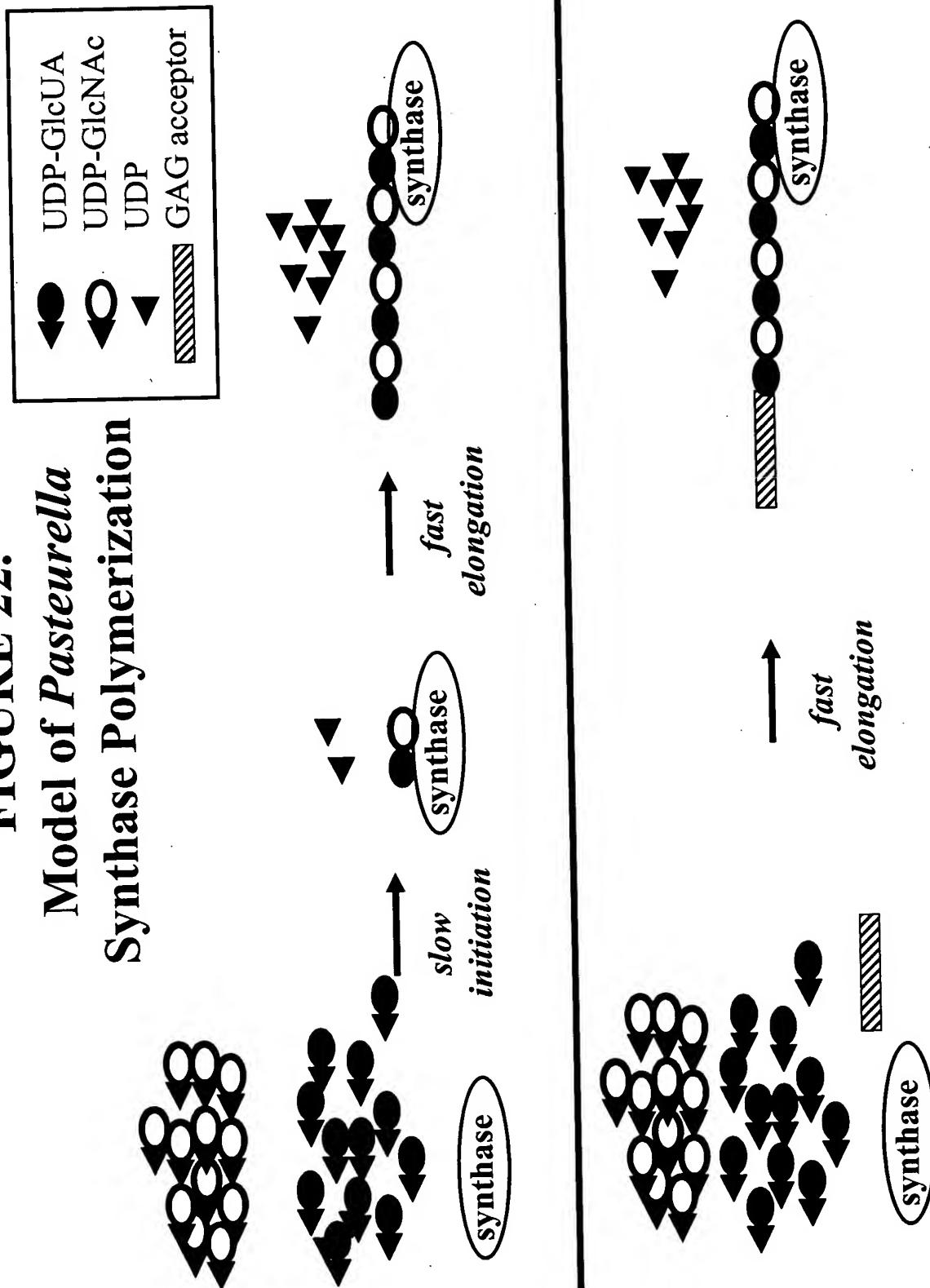


FIGURE 23.
Model of Reaction Synchronization

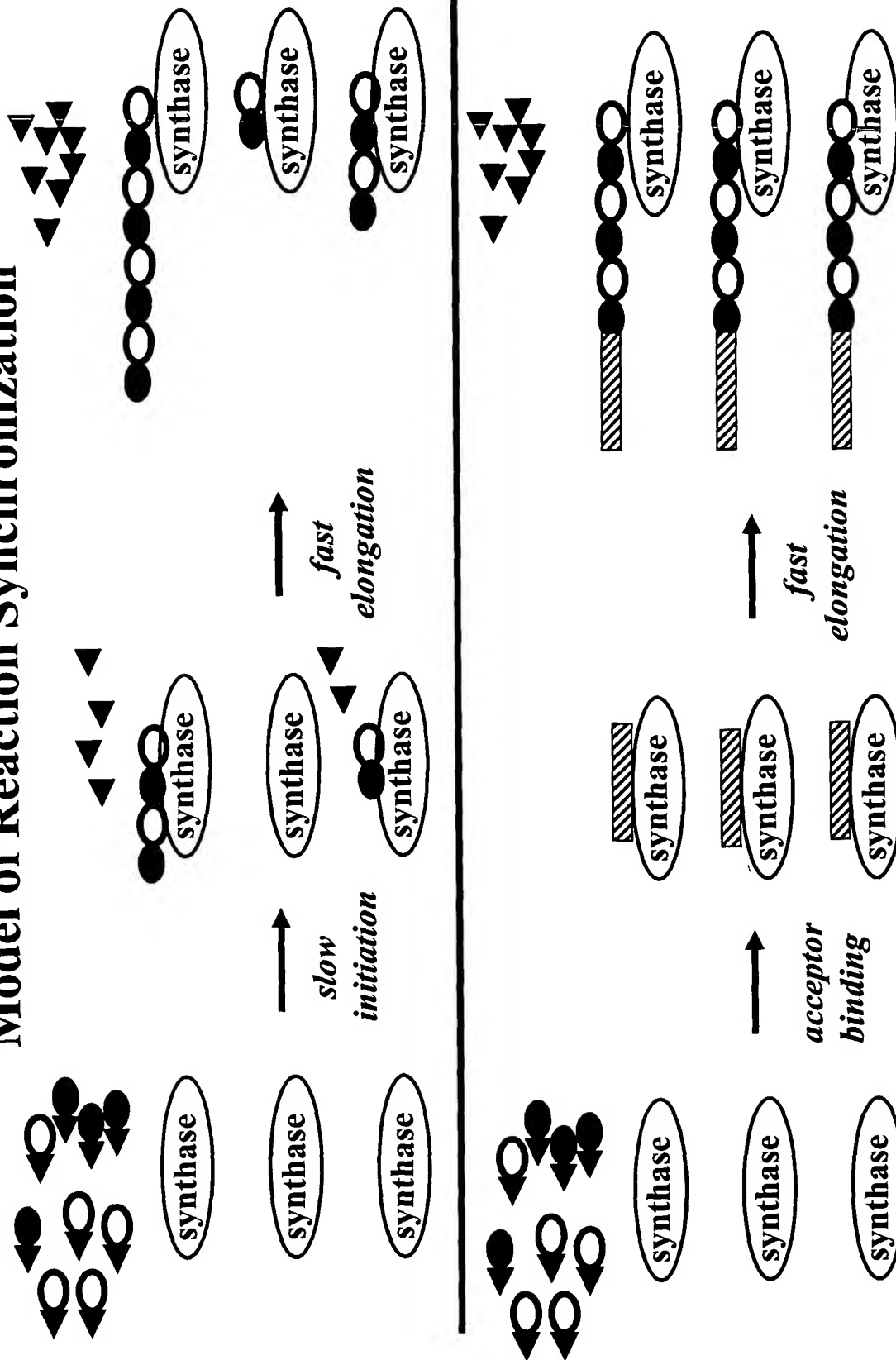


FIGURE 24.
Model of Stoichiometric Control of Polymer Size

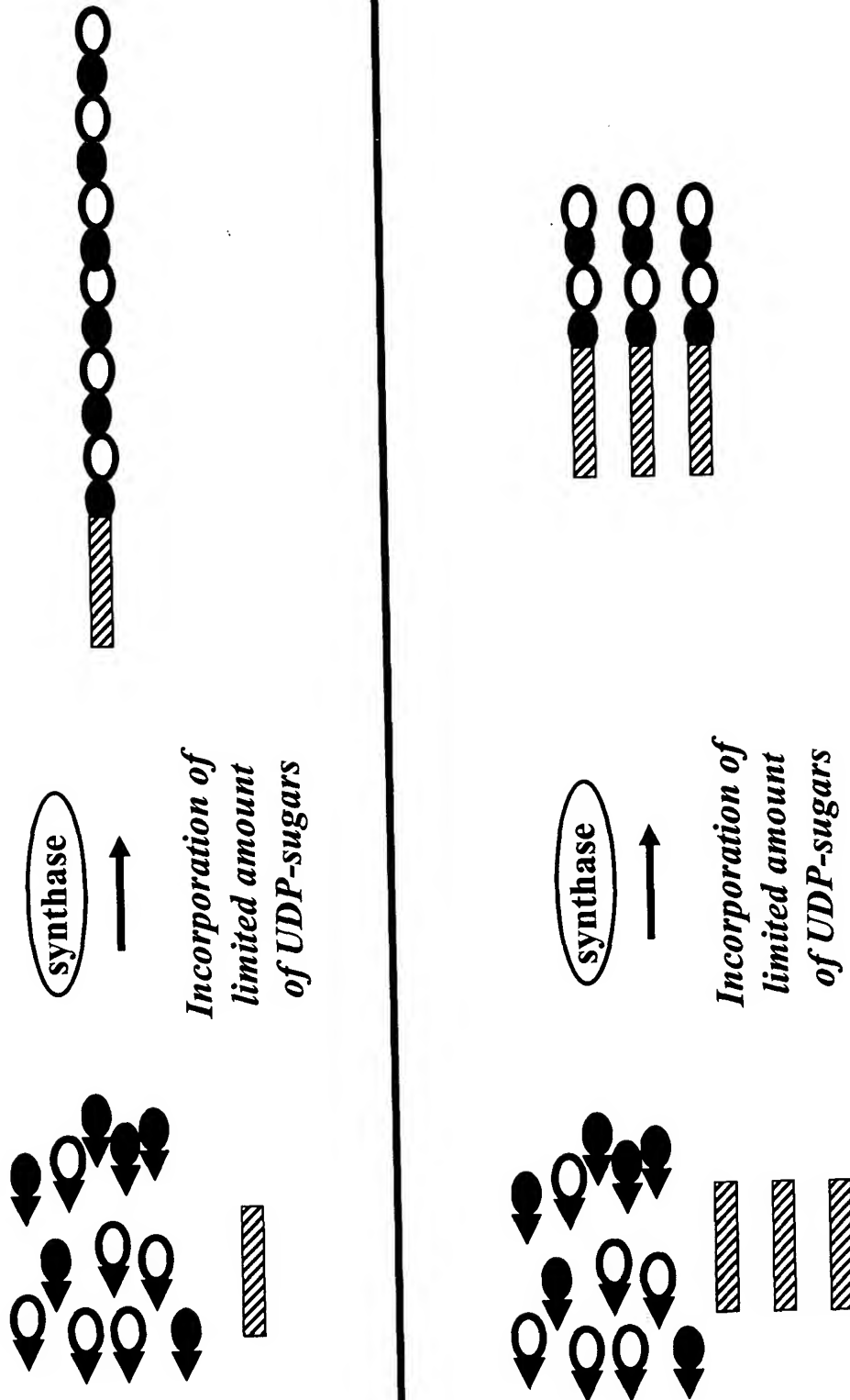


FIGURE 25

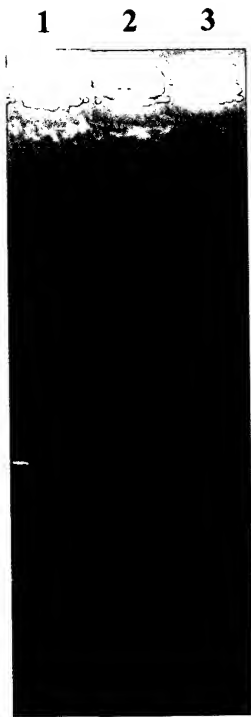
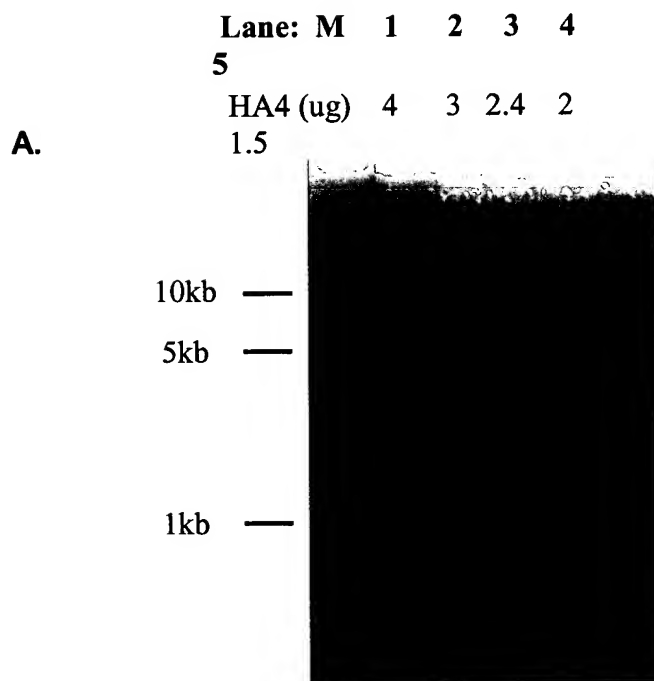


FIGURE 26



B.

Sample No	<i>M_n</i>	<i>M_w</i>	polydispersity
#1	283400	283800	1.001
#2	346400	347000	1.002
#3	422200	423700	1.004
#4	490000	493100	1.006
#5	569700	575200	1.010

FIGURE 27

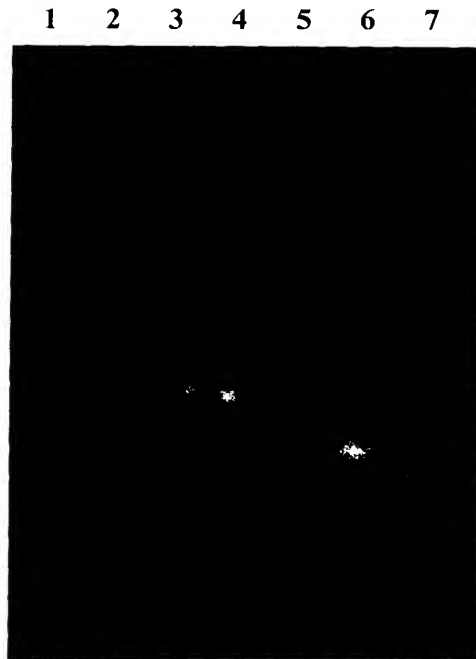


FIGURE 28

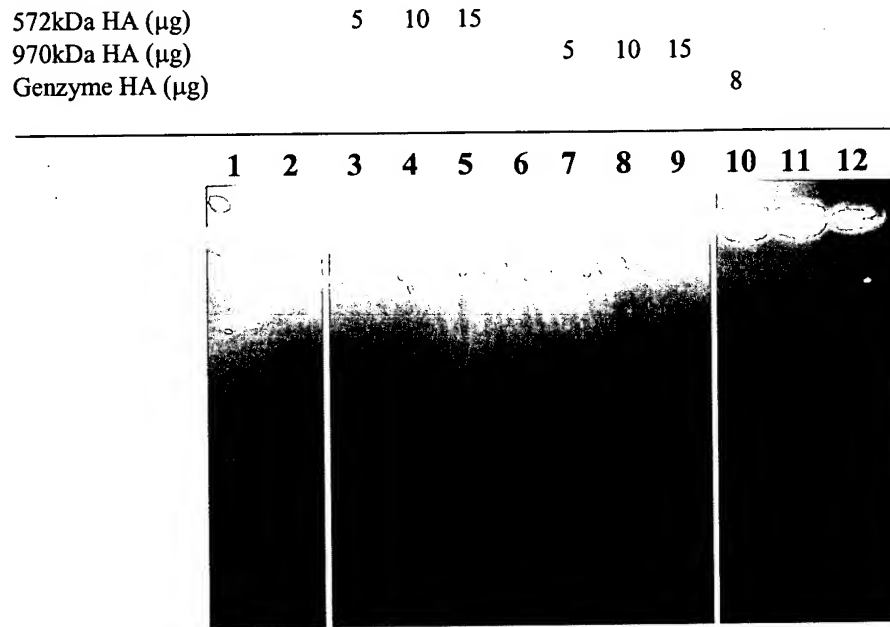


FIGURE 29.
Agarose Gels of Ladders and Migration

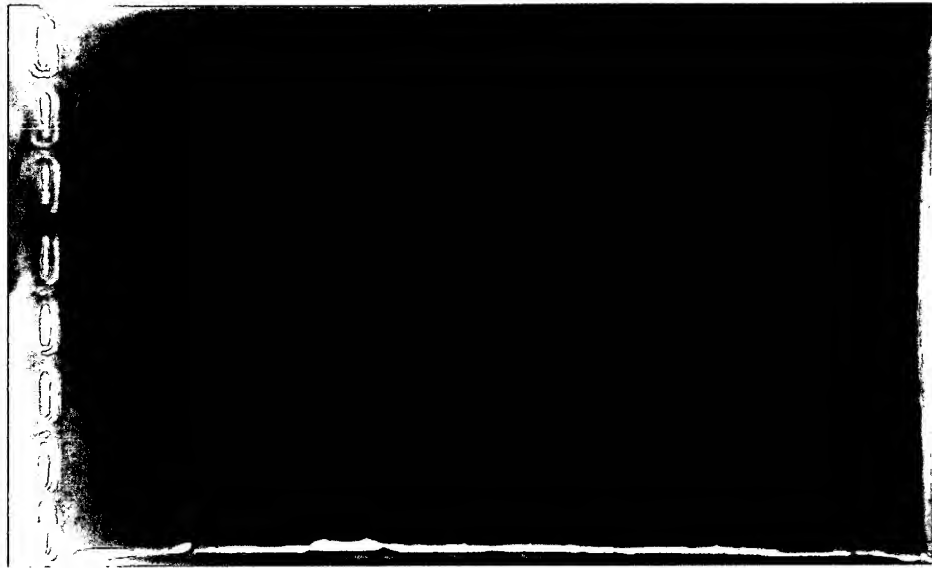
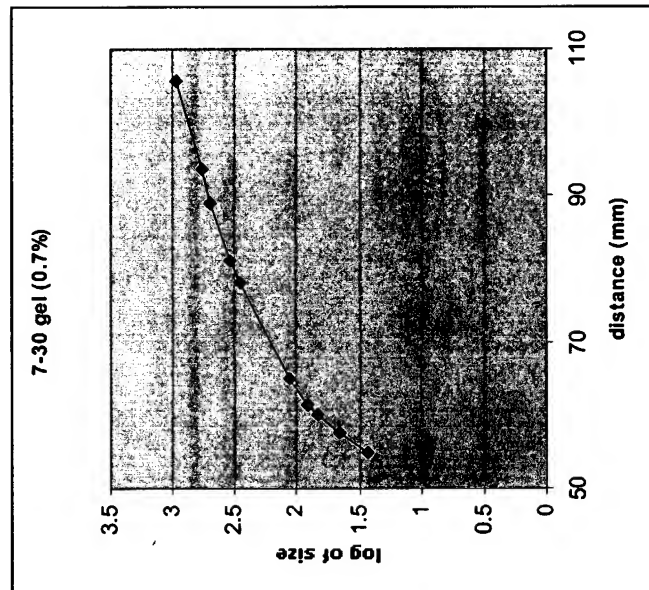


FIGURE 30

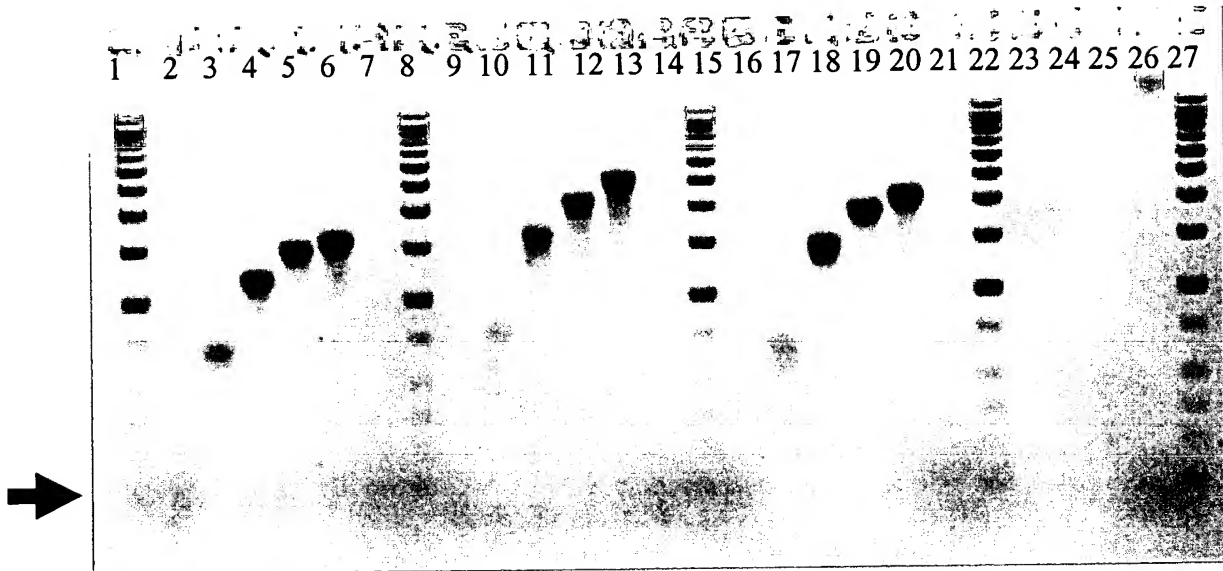


FIGURE 31

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26

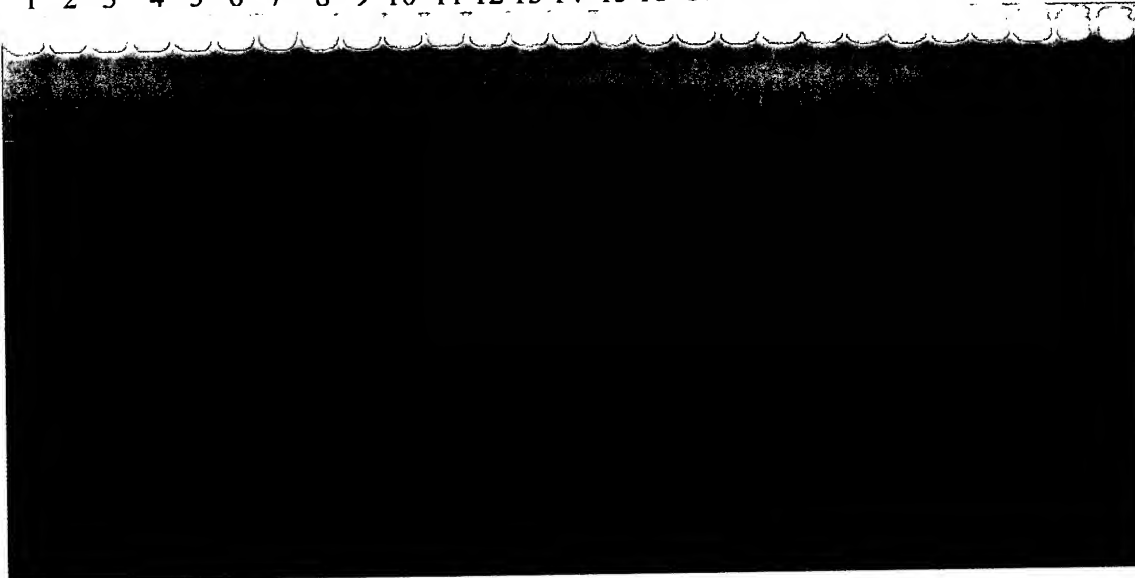
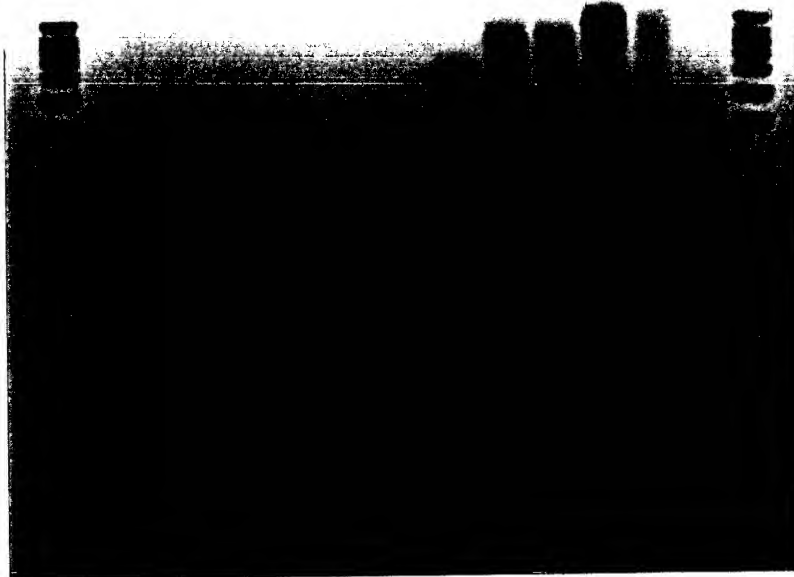


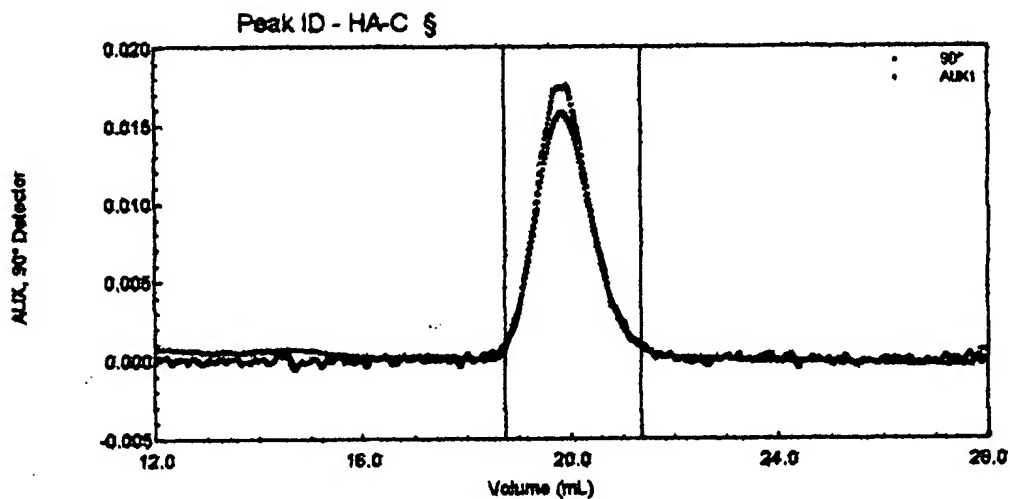
FIGURE 32



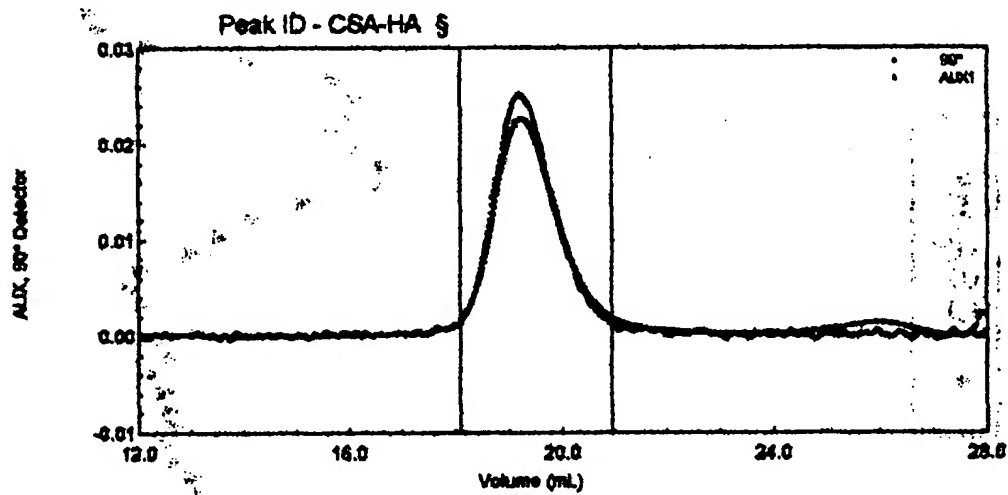
Time: 0 2 4 4 6 O/N 0
Feeding round: - 1 2 1 3 3 -

FIGURE 33

A.



B.



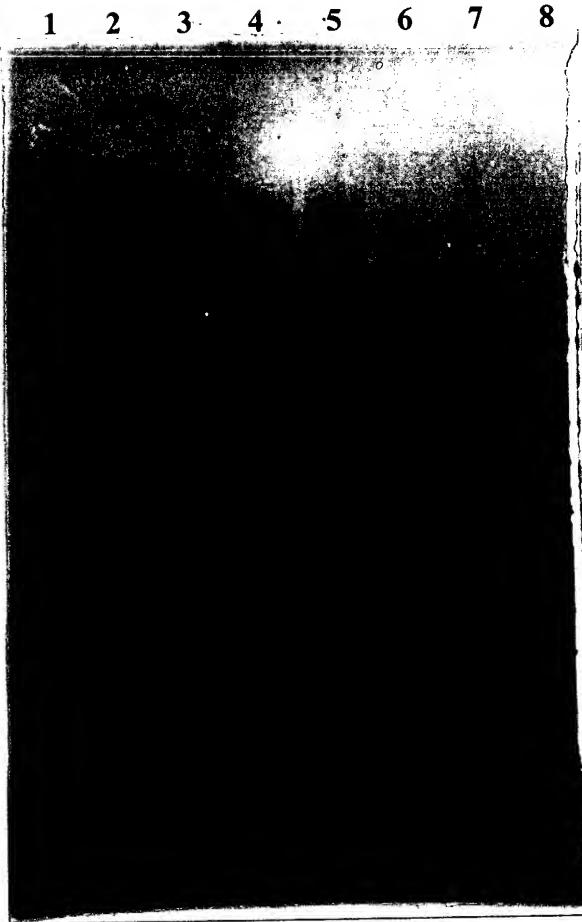


FIG. 34